

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 19:40:25 ; Search time 1774.61 Seconds  
(without alignments)  
5932.360 Million cell updates/sec

Title: US-09-597-771-11

Sequence: 1 aaagaatcctagagagagaa.....gcataaaaaaaaaaaaaa 780

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_estin:\*  
3: em\_estin:\*  
4: em\_estin:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	707.4	99.7	736	10	BG126997
2	695.2	89.1	761	10	BG128621
3	660.4	84.7	692	10	BG129599
4	632.4	81.1	703	10	BM111265
5	632.4	81.1	708	10	BM408093
6	630.8	80.9	708	10	BI179266
7	617.4	79.2	708	10	BI433851
8	617.4	79.2	646	9	BF113889
9	616.4	79.0	646	9	AM621798
10	613.8	78.7	637	9	AT491151
11	612.2	78.5	654	9	AM622132
12	605.8	77.7	624	10	BI203884
13	603.2	77.3	622	10	BI205158
14	588.4	75.4	617	10	BE451409
15	579.8	74.3	645	10	BG590355
16	578.4	74.2	636	10	BG131118
17	573.4	73.5	694	10	BF460225

18	566.8	72.7	624	10	BG600393	BG600393	EST505288
19	560.4	71.8	599	9	AM649591	AM649591	EST228045
20	558	71.5	613	10	BG598608	BG598608	EST503508
21	557.6	71.0	600	9	AM650303	AM650303	EST328757
22	553.6	71.0	607	10	BI432185	BI432185	EST534946
23	541.4	69.4	552	9	AM039483	AM039483	EST281764
24	536.8	68.8	586	10	BG598846	BG598846	EST1903746
25	535	68.6	635	10	BG589422	BG589422	EST497264
26	529.8	67.9	549	9	AM219868	AM219868	EST302351
27	529.4	67.7	547	9	AM621943	AM621943	EST312741
28	528.4	67.7	550	9	AT781299	AT781299	EST262178
29	522	66.9	549	10	BI208112	BI208112	EST526152
30	518.8	66.5	568	10	BM112206	BM112206	EST559742
31	518	66.4	583	10	BG890993	BG890993	EST16844
32	516.4	66.2	532	9	AT484872	AT484872	EST243133
33	516.2	66.2	544	9	AM649132	AM649132	EST327586
34	509.8	65.4	559	9	AM907082	AM907082	EST343114
35	505.8	64.8	555	10	BG098841	BG098841	EST463360
36	496.4	63.6	510	9	AM092208	AM092208	EST285304
37	492.8	63.2	518	9	AM625182	AM625182	EST319089
38	488.4	62.6	504	9	AT776147	AT776147	EST257235
39	482.4	61.8	506	9	AM094639	AM094639	EST287807
40	479.4	61.5	503	10	BF114414	BF114414	EST442004
41	479	61.4	493	10	BI209089	BI209089	EST527129
42	469.8	60.2	473	9	AM932090	AM932090	EST357933
43	461.4	59.2	477	9	AT898530	AT898530	EST267973
44	457.8	58.7	461	9	AM092305	AM092305	EST285485
45	457.4	58.6	475	10	BI434352	BI434352	EST537113

## ALIGNMENTS

RESULT 1  
LOCUS BG126997 736 bp mRNA linear EST 31-JAN-2001  
DEFINITION EST472643 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
cTOF14G7 5' sequence, mRNA sequence.  
ACCESSION BG126997  
VERSION BG126997.1 GI:12627185  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
REFERENCE 1 (bases 1 to 736)  
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,  
Hansen,C., Ronning,C. and Tanksley,S.  
TITLE Generation of ESTs from tomato shoot/meristem tissue  
JOURNAL Unpublished (2001)  
COMMENT Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.  
Location/Qualifiers

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/organism="Lycopersicon esculentum"  
/cultivar="T496"  
/db\_xref="taxon:4081"  
/clone="cTOF14G7"  
/clone\_id="tomato shoot/meristem"  
/tissue\_type="shoot/meristem"  
/dev\_stage="developing shoots from 4-6wks old plants"  
/lab\_host="SOLR"  
/note="Vector: pluscript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Small expanding leaves from the growing tip were  
taken from greenhouse plants (4-6wks old T496). Tissue  
was immediately frozen in liquid nitrogen."  
BASE COUNT 221 a 136 c 165 g 214 t

ORIGIN



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Db 623 ACTAGATTAATACTGTGTATTGCTACTGTTCAAAAAGAAAGAAAGAAAGCTCTGTA 682
QY 658 tggctagagaagaatttgcttgagcttgcagacagctgaactaigtgaattc 717
Db 683 TGGCTAGAGAAAGTATGGCTTTGAGCTTTT-ACAGCAGCACTGTAACATATGTGAAATTC 741
QY 718 tacttttttttttctg99 735
Db 742 TACTTTTTTTTTTTTTTGG 759

RESULT 3
Bg129599 692 bp mRNA linear EST 31-JAN-2001
LOCUS EST475245 tomato shoot/meristem Lycopersicon esculentum cDNA clone
DEFINITION ctop25E23 5' sequence, mRNA sequence.
ACCESSION Bg129599
VERSION Bg129599.1 GI:12629787
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 692)
AUTHORS Van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Konning,C. and Tanksley,S.
TITLE Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES
source
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location/Qualifiers
/organism="Lycopersicon esculentum"
/cultivar="T4496"
/db_xref="taxon:4081"
/clone="ctop25E23"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old T4496). Tissue
was immediately frozen in liquid nitrogen."
BASE COUNT 213 a 133 c 158 g 188 t
ORIGIN
Query Match 84.7% Score 660.4; DB 10; Length 692;
Best local Similarity 99.4%; Pred. No. 7e-117; Indels 3; Gaps 2;
Matches 664; Conservative 0; Mismatches 1;
QY 30 tagagagagaagcatgtcgacgaagaacacatttgatgcaagcagatgctgtgc 89
Db 2 TAGAGAGAGAGCATGTGCGAGCAGAGAACACCATTTTGAAGCAAGGAGATGCTGGTGC 61
QY 90 cttaaaaactttccacagcaagctggaacacatcgtaagaatggttcacgtatcaaa 149
Db 62 CTAAAAAACTTTCACACAGCAAGCTGGAACTCCGTAAGATGGTTACATCGTTATCAA 121
QY 150 aggcgcgtccctcgaagtggtgtgagctccactcaaaactggaacacgagacatgc 209
Db 122 AGGCCGTCCTGCAAGCTGTGAGGCTTCACACTTCAAAACTGCAAGACGAGCATGC 181
QY 210 taatgtcactttgtggaacttgacatttcaatgaaagaactggaagatacgttcc 269
Db 182 TAAATGTCACTTGTGGCAATTGACATTTTCAATGGAAAGAAACTGGAAGATATCGTTCC 241

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QY 270 gtcctccacaatttgatgtgtgcacatgtaaccgtaccgactatcagctgattgatat 329
Db 242 GTTCCTCCCACTATTGTGATGTGCGACATGTTAACCGACATATAGCTGATTGATAT 301
QY 330 ctctgaagaatggtttgtctcaactcttactgaagaagtgaacacaaagatgaacctag 389
Db 302 CTTGAGAGATGGTTTGTCTCAGCTTTACTTACGAAAGTGGAACACCAAGATGACCTCAG 361
QY 390 gcttcccaacgataaatactgctgaagcaggttaagaatggtgtcagaagaagaagga 449
Db 362 GCTTCCACCGATGAATAATCTGCTGAAGCAGATTAAAGATGGTTCCAGGAAGGAAGA 421
QY 450 tcttggtgtctgtatgctgctgcgatggtggaagagacagatlaacgcgtlaagagat 509
Db 422 TCTTGGGTGTGTGTATGTGTCGATGGCGAAGACAGATTAACGCCGTTAAGATGT 481
QY 510 tggtaacagaatttgatgtatgtcatgagcagc--ataatcactgccaagcttaagacat 567
Db 482 TGGTACCAAGAAATTGATTATGTGTCATGCGACATTAATCACTGSCAAAGCTTTAAGCAT 541
QY 568 tatcatctctaattgtgttacttgatatactacatgattataaactggttattgcaatg 627
Db 542 TATCATATCTTAATGTGGTACTTGTATATCACTAGATTATTAAGTGTATTGCACTG 601
QY 628 ttcaaaacaaagaagaagaactgctgttatggtctagaagaagatggtcttgagcttt 687
Db 602 TTCAAAACCAAAAGAAAGAAAGAACTGCTGTTATGGCTAGAGAAAGATTGGCTTTGAGCTTT 661
QY 688 tgacagcagctgtaacatgtgaaat 715
Db 662 TG-CAGCACAGTTGAACATATGTGAAAT 688

RESULT 4
Bm11265 703 bp mRNA linear EST 26-NOV-2001
LOCUS EST558801 potato roots Solanum tuberosum cDNA clone cPRO10F18 5'
DEFINITION end, mRNA sequence.
ACCESSION Bm11265
VERSION Bm11265.1 GI:17073666
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 703)
AUTHORS Van der Hoeven,R., Sun,H., Karanycheva,S.A., Tsai,J., Van Aken,S.,
Utterback,T., Chlemingo,A., Bougri,O., Buell,C.R., Konning,C.,
Tanksley,S. and Baker,B.
TITLE Generation of ESTs from potato roots
JOURNAL Unpublished (2001)
COMMENT Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: Please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.
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source
1..703
location/Qualifiers
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPRO10F18"
/clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; supplier: Cornell University, Tanksley lab;
sequencing: The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium."

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Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

BASE COUNT 218 a 143 c 158 g 184 t  
ORIGIN

Query Match 81.1%; Score 632.4; DB 10; Length 703;  
Best Local Similarity 95.9%; Pred. No. 1.6e-111;  
Matches 660; Conservative 0; Mismatches 26; Indels 2; Gaps 1;

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QY 20 aagggaatcctagaagaagacatgctgcgaagaaacacatttgaagtcagaagcag 79
DB 1 AAGGGATCCTTAGAGAGAGAGACATGTGGAGAGAACACCATTTTGAACAAAGCGC 60
QY 80 atgctggtgctcctcaaaaacttcccaagcagcagtcggaacatccgttaagaattgta 139
DB 61 ATGCTGCTGCTCAAAAACCTTACCCACAGCAAGCTGGAACCATCCGTAAGATGTTACA 120
QY 140 tggatataaagccgtccctcgaagttgttgaagttcccaactcaaaaactggaagac 199
DB 121 TCGTTATCAAAAGCCGCTCCCTCAAGGTTGTTGAGGTCTCCACTTCAAAAACCTGGAAGC 180
QY 200 acggaacatgctaagtgcacttctggaacattgcaatttcaatggaaagaactggaag 259
DB 181 ACGGACATGCTAAATGCTACTTTGTGGCAATTGACATTTTCAATGGAAGAAACCTCGAAG 240
QY 260 atatgcttcgctcccccacaaattgtatgtgccacatgtaacgctccgaactacagc 319
DB 241 ATATTCGTTCCATCCCTCCCAATGTGACGTGCCACATGTCACCGTACCGCATATCAGC 300
QY 320 tgaatatactctggaagatgtttgtctcaactcttactgaagtggaacaccaaag 379
DB 301 TGAATTACATCTCTGAAGATGTTGTGTCTCCCTTCTTACTGAAGTGGAAACACCAAGG 360
QY 380 atgacctcagcgttccaccagatgaaatctgctgaagcaggctaaagaatggttcag 439
DB 361 ATGACCTCGGCTCCACCGATGGAAGTCTGCTGAAGCAGGTAAAGTGGTTCAGG 420
QY 440 aaggaaagacatctgtgtgtctgtatgtctgcgaatggcgaagacagatatacgcag 499
DB 421 AAGGAAGAGTCTTGTGGTGTCTGTATGTCTGCGATGGCCAGAGACGATTAATGCCA 480
QY 500 ttaaggaatgtgttaccaagaattgtaatgtaacatgagcagcat--aatcactgcgaagc 557
DB 481 TTAAGGATATGTGTACCAAGAAATTAGTTGGCGCGACATCAATAATCAGTCCAAAGC 540
QY 558 ttaagaacatcatcatcctaagtgtgtaacttgaatcactagaattataaactggtt 617
DB 541 TATTAAGCATCATTAATATCTTAATGTGGTACTTTGATATCATTAGATTAATAACTCTGT 600
QY 618 atttcacgtcttcaaaaagaagaagaagaactgctgttatagtgctagaagaatgtgc 677
DB 601 ATTTCGCTTTGAAAACAAAAGAAAACCTGCTGCTATGCTGAGAAAGTATTTGCG 660
QY 678 ttgaagcttttgacagcacagtgaact 705
DB 661 TTTCAGCTTTTGACAGCACAGTTGAAGT 688
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RESULT 5  
LOCUS BM408093 708 bp mRNA linear EST 22-JAN-2002  
DEFINITION EST582420 potato roots Solanum tuberosum cDNA clone cPRO3307 5' end  
ACCESSION BM408093  
VERSION BM408093.1 GI:18259723  
KEYWORDS EST.  
SOURCE Solanum tuberosum  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 708)

AUTHORS van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,  
Utterback,T., Chleminigo,A., Bougri,O., Buell,C.R., Romning,C.,  
Tanksley,S. and Baker,B.  
JOURNAL Generation of ESTs from potato roots  
COMMENT Unpublished (2001)  
Contact: Research Genetics, Libraries Division  
Tel: 1-800-711-6195  
Email: cdna@resgen.com  
For clone info: please contact Research Genetics, Libraries  
Division tel.1-800-711-6195, email cdna@resgen.com  
Seq primer: T3

FEATURES  
source Location/Qualifiers  
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/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="cPRO3307"  
/clone\_lib="potato roots"  
/tissue\_type="roots"  
/dev\_stage="in vitro grown stem cuttings"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; supplier: Cornell University, Tanksley lab;  
sequencing: The Institute for Genomic Research. Roots were  
isolated from in vitro grown stem cuttings on CM medium.  
Roots were isolated two weeks after placing the stem  
cuttings from in vitro grown plants on medium."

BASE COUNT 219 a 142 c 158 g 189 t  
ORIGIN

Query Match 81.1%; Score 632.4; DB 10; Length 708;  
Best Local Similarity 95.9%; Pred. No. 1.6e-111;  
Matches 660; Conservative 0; Mismatches 26; Indels 2; Gaps 1;

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QY 20 aagggaatcctagaagaagacatgctgcgaagaaacacatttgaagtcagaagcag 79
DB 1 AAGGGATCCTTAGAGAGAGAGACATGTGGAGAGAACACCATTTTGAATCAAAAGCGC 60
QY 80 atgctggtgctcctcaaaaacttcccaagcagcagtcggaacatccgttaagaattgta 139
DB 61 ATGCTGCTGCTCAAAAACCTTACCCACAGCAAGCTGGAACCATCCGTAAGATGTTACA 120
QY 140 tggatataaagccgtccctcgaagttgttgaagttctcacttcaaaaactggaagac 199
DB 121 TCGTTATCAAAAGCCGCTCCCTCAAGGTTGTTGAGGTCTCCACTTCAAAAACCTGGAAGC 180
QY 200 acggaacatgctaagtgcacttctggaacatttcaatgtaagaagaactggaag 259
DB 181 ACGGACATGCTAAATGTCATCTTTGTGGCAATTGACATTTTCAATGGAAGAACTGCGAAG 240
QY 260 atatgcttcgctcccccacaaattgtatgtgccacatgtaacatgtaacgtaacgatacagc 319
DB 241 ATATGCTTCATCCCTCCCAATGTGACGTGCCACATGTCACCGTACCGCATATAGC 300
QY 320 tgaatatactctgaagaatggtttgtctcactcttactgaagaatggaagaaccaaag 379
DB 301 TGAATGACATCTCTGAAGATGTTGTGTCTCCCTTCTTACTGAAGTGGAAACACCAAG 360
QY 380 atgacctcagcgttccaccagatgaaatctgctgaagcaggttaagaatggttcag 439
DB 361 ATGACCTCGGCTTCCACCGATGGAAGTCTGCGAAGCAAGTAAAGATGGTTCCAGG 420
QY 440 aaggaaagatctgtgtgtctgtatgtctgcgaatggcgaagagaagaattgaagcag 499
DB 421 AAGGAAGAGTCTTGTGGTGTCTGTTATGCTGCGCATGGGGAAGAGCAGATTAATGCCA 480
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QY 558 ttaagaacatcatcatcctaagtgtgtaacttgaatcactagataactggtt 617
DB 541 TATTAAGCATCATTAATATCTTAATGTGGTACTTTGATATCATTAGATTAATAACTCTGT 600
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Db 541 TATAGACATTATATATCTATATGTAATTGTAATCTAGTACATGTAATCTCTGT 600

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Db 601 ATTTGACACTGTTGAAAACAAAAGAAAACGTGCTGTAGTGAAGAATGTGSC 660  
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QY 678 tttagctttgcagcacagttagact 705  
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Db 661 TTTGAGCTTTTGACAGCACAGTTGAAGT 688

RESULT 6  
BI179266  
LOCUS BI179266 708 bp mRNA linear EST 09-JUL-2001  
DEFINITION EST520211 CSTE Solanum tuberosum cdna clone cSTE1P20 5' sequence,  
mRNA sequence.  
ACCESSION BI179266 GI:14645077  
VERSION BI179266  
KEYWORDS EST.  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 708)  
van der Hoeven, R., Bezzerides, J., Bachem, C., Vissers, R., Cho, J.,  
Chiemingo, A., Bougri, O., Buell, C. R., Ronning, C., Tanksley, S. and  
Baker, B.  
Generation of ESTs from in vitro grown microtubers  
Unpublished (2001)  
CONTACT: Cathy Ronning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: M13F-R.

FEATURES  
source  
location/Qualifiers  
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/organism="Solanum tuberosum"  
/cultivar="Bintje"  
/db\_xref="taxon:4113"  
/clone="cSTE1P20"  
/clone\_lib="CSTE"  
/tissue\_type="axillary buds of stem explants; growing  
sink-tubers"  
/dev\_stage="7, 8 and 10 days"  
/lab\_host="SOLR"  
/note="vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Tissue supplied by Christian Bachem and Richard  
Vissers (Department of Plant Breeding, Wageningen  
University, The Netherlands). The cSTA libraries will  
attempt to capture the induction and initiation/initial  
growth of the tuber in an in vitro system as described in  
Bachem et al. (Plant Journal, 1996). Small microtubers  
develop from axillary buds attached to stem explants when  
placed on a high sucrose medium (10%). Visible  
morphological changes occur synchronously at day five in  
the axillary buds. The first library, cSTA (1-20) consists  
of axillary buds harvested on days 1-3. This targets  
those genes involved in induction of the microtubers. The  
following libraries, cSTA (21-40) and cSTA (41-60),  
capture genes involved in tuber initiation and outgrowth.  
This library is noted as P3 in Tanksley lab notebooks."

BASE COUNT 220 a 142 c 157 g 189 t

ORIGIN

Query Match 80.9%; Score 630.8; DB 10; Length 708;  
Best Local Similarity 95.8%; Pred. No. 3.2e-111;  
Matches 659; Conservative 0; Mismatches 27; Indels 2; Gaps 1;

QY 20 aaggaatcctcagagagcagcatgtgcgcgaagaacaccattttagtccaagcgag 79  
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Db 1 AAGGAACTCTTAGAGAGAGCATGTGAGAGAAACACCACTTTGTAGTCAAGGCGAG 60

QY 80 atgctgctgcctcaaaaacttccacagcagctggaaaccatccgtaagaatggttaca 139  
|||||  
Db 61 ATGCTGTGCTCTCAAAAACCTTACCACAGCAAGCTGGAGACCATCCGTAAGATGGTTACA 120  
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QY 140 tcgtatcaaaagccgctccctgcgaagtgtgttgaggtctccacttcaaaaactvgaaac 199  
|||||  
Db 121 TCGTTATCAAAAGCCCGTCCCGCAAGGTTGTGAGGCTCCACTTCAAAAACCTGGAAGC 180  
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QY 200 aaggaatcgtcaaatgtcactttgtgcgaatgtgacatttcaatggaaagaacttggag 259  
|||||  
Db 181 ACGGACATGCTAAATGTACTTTGTGGCAATGTGCAATTTTCAATGGAAGAATCTCGAAG 240  
|||||

QY 260 atatogtccgctccctcccaaatgtgatagtgcacatgttaaccgttaccgactatcagc 319  
|||||  
Db 241 ATATGCTGTCACTCCCTCCCAATGTGTGACGTCACATGTCAACGTAAGTACTATCAGC 300  
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QY 320 tgattgatatctcgaagatgtgtttgttctacttcttactcgaagtggaaacccaag 379  
|||||  
Db 301 TGATTGACATCTGTGAAGATGTTTGTCTCCCTTACTGAAAAGTGAAACACCAAGG 360  
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QY 380 atgacctgaagcttcccaacgcatgaaaatcgtcgaagcaggttaagaatggttccag 439  
|||||  
Db 361 ATGACCTCGGCTTCCACCGATGAAGTGTGCTGAAAGCAAGTTAAAGATGGTTCCAGG 420  
|||||

QY 440 aaggaagaagatcctgtgtgtctgtctgtatgtctgcgatggcggaagacagattaacgcg 499  
|||||  
Db 421 AAGGAAAGATCTGT 480  
|||||

QY 500 ttaagagatgtgtgaccagaagattgtaigtacatgacagcat--aatcactgccaagc 557  
|||||  
Db 481 TTAAGGATTTGTGTAACCAAGATTAGTTGTGCCGCGACATCATTAATTCACCTGCCAAGC 540  
|||||

QY 558 ttaagaatatacatatcctaattgtgtactttagatatacaatgataaactgtgt 617  
|||||  
Db 541 TATAAGACATCATATATATCTTAATGTGTGTAATGTGTGTAATGTGTATTAATTAATCTGTT 600  
|||||

QY 618 attgcactgttcaaaaacaaagaactgctgttatggttagagaagtattggc 677  
|||||  
Db 601 ATTTGACACTGTTGAAAACAAAAGAAAACGTGCTGTAGTGAAGAATGTGSC 660  
|||||

QY 678 tttagctttgcagcacagttagact 705  
|||||  
Db 661 TTTGAGCTTTTGACAGCACAGTTGAAGT 688

RESULT 7  
BI433851  
LOCUS BI433851 708 bp mRNA linear EST 21-AUG-2001  
DEFINITION EST536599 P. Infestans-challenged leaf Solanum tuberosum cdna clone  
PCR8J11 5' sequence, mRNA sequence.  
ACCESSION BI433851 GI:15258528  
VERSION BI433851  
KEYWORDS EST.  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 708)  
Restrepo, S., Griffiths, H. M., Smart, C. D., Cho, J., Chiemingo, A.,  
Bougri, O., Buell, C. R., Ronning, C. M., Fry, W. E. and Baker, B.  
Generation of ESTs from Potato Leaves Challenged with Phytophthora  
Infestans, Compatible Interaction  
Unpublished (2000)  
CONTACT: Cathy Ronning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: M13F-R.

FEATURES  
source  
location/Qualifiers  
1..708  
/organism="Solanum tuberosum"

```

/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PCB311"
/clone_lib="P. infestans-challenged leaf"
/tissue_type="Leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; Whole plants were challenged with 450,000
sporangia/ml P. infestans US-1(US 940501) in Blottron
(Madison, Wisconsin). Leaf tissue was collected at 1, 2,
5, 12, and 24 hours post-challenge and frozen in liquid
nitrogen immediately upon removal. Kennebec plants showed
no signs of HR. Kathadin plants (susceptible to P.
infestans US-1) were used as controls and showed
infection. NOTE: We cannot exclude the possibility that
this sequence is actually derived from Phytophthora rather
than potato."

```

```

BASE COUNT      218 a      143 c      160 g      187 t
ORIGIN
Query Match      79.2%; Score 617.8; DB 10; Length 708;
Best Local Similarity 94.5%; Pred. No. 9.9e-109;
Matches 674; Conservative 0; Mismatches 32; Indels 7; Gaps 3;

```

```

QY 20 aaggaatcctagaagaagaacatgctgcgaagaacacacatttgaagcaagcag 79
DB 1 AAGGAAATCTTAGAGAGAGAGCATGTGGACGAGAACACCAATTTTGAAGTAAAGCGCAG 60
QY 80 atgctgtgctcctcaaaactttccacagaagctggaacacatccgtlaagaattggtaca 139
DB 61 ATGCTGTGCTCTCAAAAACATTACCCACAGCAGTGAACCATCCGTAGAGATGGTTACA 120
QY 140 tegtatacaaggcgtccctcgaagtggtggaagctccctccatcaaaacttgtaaac 199
DB 121 TCGTTATCAAAAGCCCTCCCTGCAAGTTGTGAGGCTCCCACTTCAAAAACCTGGAAAC 180
QY 200 acgagacgtgtaaatgtaactctgtgcaattgacatttcaaatggaagaacgtgaag 259
DB 181 ACGGACATGCTAAATGCTACTTGTGCAATTTGACATTTGAAAGAAACCTCGAAG 240
QY 260 atatgcttcgctcccccacaactgtgatgtgcacatgttaacgctacgaactatcagc 319
DB 241 ATATCGTTCATCTCCCTCCCAATTTGACGTGCGACATGTCAACCTACCGCATATCACG 300
QY 320 tegtatactctggaagtggttgtgtctcacttcttcaaatggaagaacacgaag 379
DB 301 TGAATGACATCTCTGAAGATGGTTGTCTCCCTTCTTACTGAAAGTGAACACCAAGG 360
QY 380 atgacctcaggtctccacacgaatgtaaatctgctgaagaagcttaagaatggttccag 439
DB 361 ATGACCTCGCGCTTCCACCGATGAAGTCTGCTGAAGCAGGTTAAAGATGGTTCCAGG 420
QY 440 aaggaagaagatcttctgtgtgtctgtatgtctgcatgtggcgaagacgaatgaacgcg 499
DB 421 AAGGAAGAGATCTTGTGTGTCTGTATGTCTGCGATGGCGCAAGCAGATTAAGGCCA 480
QY 500 ttaagaatgtgttacaagaatagtatgtcatatgtagcagcat--aatcagcccaagc 557
DB 481 TTAAGGATATTTGGTACCAAGATTAATGATGCGCGCATCAATAAATCAGTCCCAAGC 540
QY 558 ttaagaatcatatcatcctaagtgtgtaacttgaatacactagataaactgtgtt 617
DB 541 TATTAAGCATTTATATATCTTAATGTGTGATCTTTGATATCAGTATTAACCTCTGTGT 600
QY 618 atttgacatgttcaaaaagaagaagaacgtggtatagctgtaagaagaagttgtgc 677
DB 601 ATTTGCACTGTTGAAGAAAGAAAG-AAAATGCTGCTATGGCTTAGAAGAAATATTTGC 659
QY 678 tttagaactttgacagacagtgtaactatgttgaatcctacttcttctt 730
DB 660 TTTGAGCTTTTGAAGCAGCAGTTGA---GTGGAATCTCTACTTTAATTAT 708

```

```

RESULT      8
LOCUS      BF113889
DEFINITION EST441479 tomato root, plant at pre-anthesis Lycopersicon
ACCESSION   BF113889
VERSION     BF113889
KEYWORDS    EST.
SOURCE      BF113889.1 GI:10943579
ORGANISM    tomato.
REFERENCE   Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS     Liang,F., Craven,M.B., Bowman,C.L., Ronning,C.M., Niernan,W.,
            Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
            Generation of ESTs from tomato root tissue, pre-anthesis stage
            Unpublished (2000)
TITLE       JOURNAL
COMMENT     Contact: CUCI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES
SOURCE
1. 646
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
/clone="cley23E19"
/clone_lib="tomato root, plant at pre-anthesis"
/tissue_type="root"
/dev_stage="pre-anthesis stage"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY
14850)."

```

```

BASE COUNT      200 a      130 c      147 g      169 t
ORIGIN
Query Match      79.2%; Score 617.4; DB 10; Length 646;
Best Local Similarity 99.5%; Pred. No. 1.2e-108;
Matches 630; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

```

QY 1 aagaatcctagaagaagaagaatcctagaagaagaacatgctgcgaagaacac 60
DB 14 AAGAAATCTTAGAGAGAGAGCATCTTAGAGAGAAACATGTGCGAGCAAGAACAC 73
QY 61 catltgagtcanaagcagatgctgtgctcctcaaaactttccacagaagctggaac 120
DB 74 CATTTGAGTCAAAAGCGCATGTGTCCTCAAAAACCTTCCACAGCAAGCTGGAAC 133
QY 121 atcgtgaagaatgttataatcgttataaagccgctccctcgaagtggtgtgtctcc 180
DB 134 ATCCGTAAAGATGTGTATATGTAATCAAAAGCCGCTCCCTGCAAGTTGTGAGGTTCC 193
QY 181 acttcaaaacttggaacacggaacatgctaactgtcaacttctgtggaatgacatttc 240
DB 194 ACTTCAAAAACCTGGAACACGACATCTTAATGTCTATTTGGCAATTGACATTTTC 253
QY 241 aatggaagaacactggaagatcgttccgtccctcccaaatgtgtgatgtgcacatgtc 300
DB 254 AATGGAAGAAACGTGAAGATATGTTCCGTCCTCCCAATTTGTGATGTGCCACAGTT 313
QY 301 aacgttaccgacttcaactgattgatatctctgaagaatgttgtctcacttact 360
DB 314 AACCGTACCGATATCACTGATATGATATCTGTGAAGATGGTTTGTCTCACTTTACT 373
QY 361 gaaatggaacacccaagaatgacctcaggtctccacgaatgaatctgtctgaagcag 420

```

Db 374 GAAAGTGAAACCAAGGATGACCTCCAGGCTTCCACGATGAATAATCTGCTGAAGAC 433

QY 421 gtaaaagatgggtccaggaaagaaagatcttgggtgtctgtatctgtcgatggc 480

Db 434 GTTAAAGATGGGTTCAGAGAAAGGATCTTGGTGTCTGTATCTTCGATGGC 493

QY 481 gaagacagattaaagccgttaagatgttggtaacaaagattagttatgtcatggcgc 540

Db 494 GAAAGCACAATTAACGCCCTTAAGCATGTGGTACCAAGAAATTAATTATGCAATGGCAGC 553

QY 541 --ataacatcgccaagcttaagacattacatactcaatgtgtactttgatca 598

Db 554 AATTAATCACTGCGAAAGCTTAAGCATTAATCATATCTAATGTGGTACTTTGATATCA 613

QY 599 ctagattataaactgtgtattgttcacgttca 631

Db 614 CTAGATTATAACTGTGTATTGTGACAGTTTCA 646

RESULT 9

AM621798 646 bp mRNA linear EST 18-MAY-2001

LOCUS EST312596 tomato root during/after fruit set, Cornell University

DEFINITION Lycopersicon esculentum cDNA clone cLEX13114 5', mRNA sequence.

ACCESSION AM621798

VERSION AM621798.1 GI:7333445

KEYWORDS EST.

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 646)

van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Kochian,L., Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.

REFERENCE

AUTHORS

Generation of ESTs from tomato root, during and after fruit set

Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

FEATURES

location/Qualifiers

1..646

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="cLEX13114"

/clone\_1lb="tomato root during/after fruit set, Cornell University"

/tissue\_type="root"

/dev\_stage="plants during and after fruit set"

/note="Vector: pBluescript SK(-); Site1: EcoRI; Site2: XhoI; supplier: Tanksley, Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."

BASE COUNT 199 a 130 c 148 g 169 t

ORIGIN

Query Match 79.0%; Score 616.4; DB 9; Length 646;

Best Local Similarity 99.5%; Pred. No. 1.9e-108;

Matches 629; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 aagaatctatagagaagaagaatcctatagagaagaagatgtcgacaaagaacac 60

Db 15 AAAGAACTCTAAGAGAGAGAAAGGAATCTTAAAGAGAGAGCATGTGACCAAGAACAC 74

QY 61 cattttagtcacaagcagatgtgtgtcctcaaaacttccccaagcagctgaacc 120

Db 75 CATTTGAGTCAAGGACAGATGCTGTGCTCTCAAAAACTTCCACAGCAAGCTGGAAC 134

QY 121 atccgtaaagatggttacatcgttatacaaaagccgtccctcgcaaggttgttgatctc 180

Db 135 ATCCGTAAGATGGTTCATACATCGTTATFCAAAAGGCCGCTCCGCAAGGTTGTTGAGTCTCC 194

QY 181 acttcaaaacttgaaaacacgcagcatgtaaatgtactttgttgcaatgtgacatttc 240

Db 195 ACTTCAAAAACCTGGAAAGCACGACATGCTAAATGTACATTTTGGCAATTGACATTTTC 254

QY 241 aatgaaagaacacggaagatatacgttcctccctcccaattgtatgtgccaatgtt 300

Db 255 AATGAAAGAAACATGGAAGATATGTTCCGTCCTCCACAAATGTGATGTGCCACATGTT 314

QY 301 aaccgtaccgactacacgtatgtatatactctgaagaatgtgtttgtctcaacttact 360

Db 315 AACGTCACCGACTATCAGCTGATGTGATATCTGMAAGATGTTTGTCTCACATCTTACT 374

QY 361 gaaatggaaacaccacagatgacatcagcttcccaacgcatgaatctgctgaaagcag 420

Db 375 GAAAGTGGAACACCAAGATGACCTCAGGCTTCCACCATGAATAATCTGTGAAGCAG 434

QY 421 gtaaaagatgggtccaggaaagaaagatcttgggtgtctgttaltgtctgcgatggc 480

Db 435 GTTAAAGATGGGTTCAGAGAAAGGATCTTGGTGTCTGTATGTCTGGGATGGC 494

QY 481 gaagacagattaaagccgttaagatgttggtaacaaagattagttatgtcatggcgc 540

Db 495 GAAAGCAGATTAACGCCCTTAAGCATGTGGTACCAAGAAATTAATTATGCAATGGCAGC 554

QY 541 --ataacatcgccaagcttaagacattacatactcaatgtgtactttgatca 598

Db 555 AATTAATCACTGCGAAAGCTTAAGCATTAATCATATCTAATGTGGTACTTTGATATCA 614

QY 599 ctagattataaactgtgtattgttcacgttca 630

Db 615 CTAGATTATAACTGTGTATTGTGACAGTTTCA 646

RESULT 10

AT491151 637 bp mRNA linear EST 18-MAY-2001

LOCUS EST241860 tomato shoot, Cornell Lycopersicon esculentum cDNA clone

DEFINITION cLEB3K4, mRNA sequence.

ACCESSION AT491151

VERSION AT491151.1 GI:4386461

KEYWORDS EST.

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 637)

van der Hoeven,R.S., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.

REFERENCE

AUTHORS

Generation of ESTs from tomato shoot meristem

Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

location/Qualifiers

1..637

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="cLEB3K4"

/clone\_1lb="tomato shoot, Cornell"

/tissue\_type="shoot meristem"

FEATURES

source

```

/dev.stage="8 week old plants"
/lab.host="X10LR"
/note="Vector: pBK.CMV; Site_1: EcoRI; Site_2: XhoI; CLEB
-tomato Shoot Meristem EST Library. Oligo-dT primed cDNA
library made from tomato vegetative shoots including
meristems and small expanding leaves."
BASE COUNT      192 a      127 c      150 g      168 t
ORIGIN

```

```

Query Match      78.7%; Score 613.8; DB 9; Length 637;
Best Local Similarity 99.4%; Pred. No. 6.1e-108;
Matches 627; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

```

```

QY      2 aagaatcctagaagaagaagaatcctagaagaagaatcgcgacgaagaacac 61
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      7 AGGAATCCAGAGAGAGAAAGGAATCCTAGAGAGAGATGCGACGACGAACACC 66
      62 atttgaatcgaagaagaatcgtggtcctcaaaaacttcccaagaactggaacca 121
      67 ATTTGAGTCGAAGGACATGCTGCTGCCCTCAAAAACCTTCCACAGCAACTGGAAACA 126
QY      122 tccgtaagaatggttacatcgltatcaaaagccgtccctgaagggttgatcca 181
      127 TCCGTAGAGATGGTTACATCGTTATCAAAAGGCCGCTCCGCAAGTTGTTGAGCTTCCA 186
QY      182 cttcaaaaactggaagaagaacgacatgctaagtacattgttggaactgaatttca 241
      187 CTTCAAAAACCTGGAAGACAGGACATGCTAAATGTCATTTGTGGCAATTGACATTTTCA 246
QY      242 atggaagaagaactggaagaatcgttcgctccctcccaacttggatgacagatgta 301
      247 AAGGAAGAAGAACTGGAAGATATCGTTCCGTCCTCCACAAATTGGATGGCACATGTTA 306
QY      302 accgtaaccgactatcagctgattgatctctgaagaatggtttgctcacttactg 361
      307 ACCGTACCGACTATCAGCTGATGATATCTGTGAAGATGTTGTCTCACTTTCTACTG 366
QY      362 aagatggaagaacccaagaatgacctcaggtctccacgaatgaaatctgtctgaacag 421
      367 AAGTGGAAACCCAAAGATGATGCTCAGGCTTCCACCGATGAAATGCTGTGAAGCAGG 426
QY      422 ttaaaagtgtggttcagaagaagaagaatcttgtgtgtctgtatgtctgagatggcg 481
      427 TTAAGATGTGGGTTCCAGAGAAAGGATCTGTGTGTCTTATGTCTGATGGGCG 486
DB      482 aagaacaatgaacgctgaagatggtgtgtaacaaatgaattgattgcatgacagc- 540
      487 AAGACAGATTACCGCCGTAAAGATGTTGGTACCAAAATTAGTTATGTATGGACAGCA 546
QY      541 -ataatcactgcgaagaatcttaagaacattacataccttaactgtgtaacttgaatcac 599
      547 TATATCACTGCCAAGCTTTAAAGCATTAATCAATATCTTAATGTGTGTTGATATCAC 606
QY      600 tagattataaactgtgtattgtacatgttc 630
      607 TAGATTATAAAGCTGTATTGTGCACTGTTC 637

```

RESULT 11

LOCUS AM622132 654 bp mRNA linear EST 18-MAY-2001

DEFINITION EST312930 tomato root during/after fruit set, Cornell University

LYCopersicon esculentum cDNA clone cLEX14G22 5', mRNA sequence.

ACCESSION AM622132.1 GI:7333779

VERSION AM622132.1

KEYWORDS EST.

SOURCE tomato.

ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanales; Solanales; Solanum;  
Lycopersicon.

```

REFERENCE      1 (bases 1 to 654)
AUTHORS      van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Kochian,L.,
      Liang,F., Hansen,T.C., Craven,M.B., Bowman,C.L., Ronning,C.M.,
      Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J., and Tanksley
      ,S.D.
      Generation of ESTs from tomato root, during and after fruit set
      Unpublished (1999)
      Contact: CUGI
      Clemson University Genomics Institute
      Clemson University
      100 Jordan Hall, Clemson, SC 29634, USA
      Email: http://www.genome.clemson.edu/orders/index.html
      5 prime sequence.
FEATURES
      source      Location/Qualifiers
      1..654
      /organism="Lycopersicon esculentum"
      /cultivar="74A96"
      /db_xref="taxon:4081"
      /clone="cLEX14G22"
      /clone.lib="tomato root during/after fruit set, Cornell
      University"
      /issue-type="root"
      /dev-stage="plants during and after fruit-set"
      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
      XhoI; supplier: Tanksley; tissue supplied by Dave Garvin
      (USDA-ARS, Ithaca, NY 14850)."
```

```

BASE COUNT      197 a      134 c      150 g      172 t      1 others
ORIGIN

```

```

Query Match      78.5%; Score 612.2; DB 9; Length 654;
Best Local Similarity 99.1%; Pred. No. 1.2e-107;
Matches 626; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

```

```

QY      1 aagaatcctagaagaagaagaatcctagaagaagaatcgcgacgaagaacac 60
      23 AAGGAATCCAGAGAGAGAAAGGAATCCTAGAGAGAGATGCGACGACGAACACC 82
QY      61 cetttgatcgaagaagaatgctgtgtcctcaaaaacttcccaagaactggaacc 120
      83 CATTTGAGTCGAAGGACATGCTGCTGCCCTCAAAAACCTTCCACAGCAACTGGAAACC 142
QY      121 atccgtaagaatggttacatcgltatcaaaagccgtccctgcaagggttgatgagtcctc 180
      143 ATCCGTAAAGATGTTATCATCGTTATCAAAAGGCCGCTCCGCAAGGATGTTGAGGCTTCC 202
DB      181 acttcaaaaactggaagaagaacgacatgctaagtacattgttggaactgaatttcc 240
      203 ACTTCAAAAACCTGGAAGACAGGACATGCTAAATGTCATTTGTGGCATGTGACATTTTC 262
QY      241 aatggaagaagaatcgtgaatgatacgttcgctccctcccaaatgtgatagtgcacatgtc 300
      263 AATGGAAGAAGAACTGGAAGTATCGTTCCGCTCCACAAATTGTGATGTGCCACATGTT 322
DB      301 aaccgtaccgactatcagctgattgatctctgaagaatggtttgtcacttcttact 360
      323 AACCGTACCGACTATCAGCTGATGATATCTGTGAAGATGTTGTTGTCTCACTTTACT 382
QY      361 gaaagtgaagaacccaagaatgacctcaggtctccacgaatgaaatctgtctgaacag 420
      383 GAAGTGGAAACCCAAAGATGATGCTCAGGCTTCCACCGATGAAATGTGCTGGAAGCAG 442
QY      421 gttcaaatgtggttcagaagaagaagaatctgtgtgtctgtatgtctgcatgagtcgagtc 480
      443 GTTAAAGATGGTTCACGAGGAAGAGATCTGTGTGTCTTATGTCTGCGATGGGCG 502
QY      481 gaaagcagaatgaacgctgtaagaatggtgtgtgtacaaagaatgattgtatgtcatgtgcagc 540
      503 GAAGACAGATTAACCCCGTTNAGATGTTGGTACCAAAATTAGTTATGTATGTCATGCAAC 562
QY      541 -ataatcactgcgaagaatcttaagaacattacataccttaactgtgtaacttgaatcac 598
      563 ATATATCACTGCCAAGCTTTAAAGCATTAATCAATATCTTAATGTGTGTTGATATCA 622

```



QY 599 ctgattataactgtgtatttgcacgttc 630  
 ||||||||||||||||||||||||||||  
 Db 623 CTGATTATRAACTGTGTATTGCACTGTC 654

RESULT 12  
 BI203884  
 LOCUS EST521924 cTOS Lycopersicon esculentum cDNA clone cTOS3122 5' end,  
 DEFINITION mRNA sequence.  
 BI203884  
 VERSION BI203884.1 GI:14681608  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 624)  
 van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,  
 Ronning, C. and Tanksley, S.  
 Generation of ESTs from Tomato Suspension Cultures  
 Unpublished (2001)  
 CONTACT: CUGI  
 CLEMSON UNIVERSITY Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>.  
 Location/Qualifiers  
 1..624  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496, E6203"  
 /db\_xref="taxon:4081"  
 /clone="cTOS3122"  
 /clone\_1lb="cTOS"  
 /tissue\_type="suspension cultures"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Suspension cultures of L.esculentum E6203 were grown  
 in Murashige and Skoog based medium, supplemented with 15%  
 coconut milk (filter sterilized and added after  
 autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).  
 Fresh medium was added every 7 days, and cultures were  
 grown at 25 C, with 12hrs of light and continuous  
 shaking."

BASE COUNT 189 a 120 c 138 g 177 t

ORIGIN

Query Match 77.7%; Score 605.8; DB 10; Length 624;  
 Best Local Similarity 99.4%; Pred. No. 2,1e-106;  
 Matches 619; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 100 ttccacacacgaactggaacatccgttaagaatggtttacatggttatacaagccgtccc 159  
 ||||||||||||||||||||||||||||  
 Db 2 TTTCACACAGCTGGAACCATCCGTAAAGATGGTTACATGTTATTAAGGCCGCTCCC 61

QY 160 tgcgaagtgttgagggtctccacttcaaaaactggaacacgacgacgtctaaatgtcac 219  
 ||||||||||||||||||||||||||||  
 Db 62 TGCAGGTGTGAGGTCTCCACTTCAAAAACCTGGAAGACGACGATGCTTAATGTCCAC 121

QY 220 ttgttgacatgacatcttcaatggaagaacgtggaagatatacgttcgcgtccacac 279  
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QY 520 aattagttatgtcattggaagc--ataatcactgcgaagccttlaagacattatcatacc 577  
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RESULT 13  
 BI205158  
 LOCUS EST523198 cTOS Lycopersicon esculentum cDNA clone cTOS7M5 5' end,  
 DEFINITION mRNA sequence.  
 BI205158  
 VERSION BI205158.1 GI:14682882  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 622)  
 van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,  
 Ronning, C. and Tanksley, S.  
 Generation of ESTs from Tomato Suspension Cultures  
 Unpublished (2001)  
 CONTACT: CUGI  
 CLEMSON UNIVERSITY Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>.  
 Location/Qualifiers  
 1..622  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496, E6203"  
 /db\_xref="taxon:4081"  
 /clone="cTOS7M5"  
 /clone\_1lb="cTOS"  
 /tissue\_type="suspension cultures"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Suspension cultures of L.esculentum E6203 were grown  
 in Murashige and Skoog based medium, supplemented with 15%  
 coconut milk (filter sterilized and added after  
 autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).  
 Fresh medium was added every 7 days, and cultures were  
 grown at 25 C, with 12hrs of light and continuous  
 shaking."

BASE COUNT 190 a 123 c 146 g 163 t

ORIGIN

Query Match 77.3%; Score 603.2; DB 10; Length 622;



VERSION	BC590355.1	GI:13608495
KEYWORDS	EST.	
SOURCE	potato.	
ORGANISM	Solanum tuberosum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.	
ATTNORS	1 (bases 1 to 645)	
TITLE	Zhang, P., Hernandez, M., Tornqvist, C.-E., Witz, U., Loukolanov, A., Rangel, P., Haberer, G. F., Cho, J., Chelimgo, A., Bougri, O., Buell, C. R., Ronning, C. M., Helgeson, J., and Baker, B.	
JOURNAL	Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Incompatible Reaction	
COMMENT	Unpublished (2000)	
CONTACT	Contact: Cathy Ronning	
FOR CLONE INFO	The Institute for Genomic Research	
PLEASE CONTACT RESEARCH GENETICS, LIBRARIES	For clone info, please contact Research Genetics, Libraries	
Seq primer: M13F-R.	Seq primer: M13F-R.	
Location/Qualifiers	1..645	
FEATURES	source	

BASE COUNT	203 a	134 c	142 g	166 t
ORIGIN				

Query Match	74.3%;	Score 579.8;	DB 10;	Length 645;
Best Local Similarity	94.7%;	Pred. No. 1.9e-101;		
Matches 611; Conservative	0;	Mismatches 32;	Indels 2;	Gaps 1;

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QY	80	atgctgctgctccaaaaacttcccaacagaacgttgaaacacatccgtaagaatgtaca	139
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QY	140	tggttatacaagcgctccctcgtcaaggttgtttgaagctcacaattcaaaaactygaaac	199
Db	121	TCGTTATCAAAAGAGTCCCTCGCAAGGTGTTGAGGTCTCCACTTCAAAAACTGGAAAGC	180
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QY	320	tgaatgatactctgaagaatggttttctcactctcttaactgaagaatygaaacccaag	379
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Search completed: September 10, 2002, 21:09:22  
Job time: 5337 sec

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